

01/12

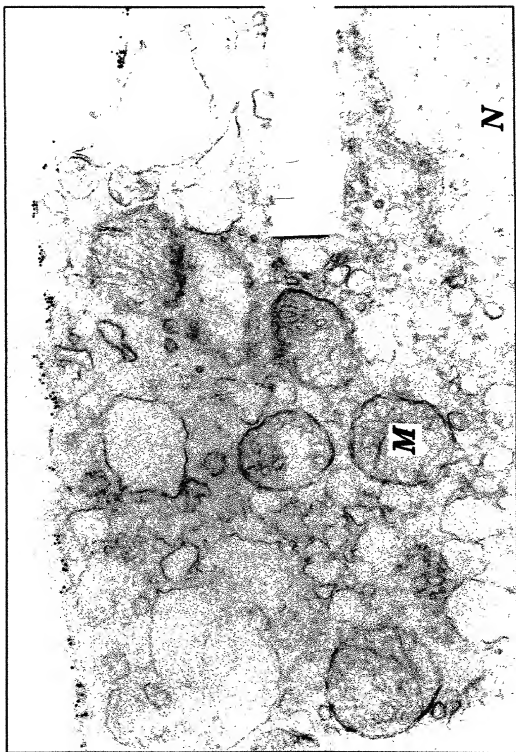


FIG. 1

02/12

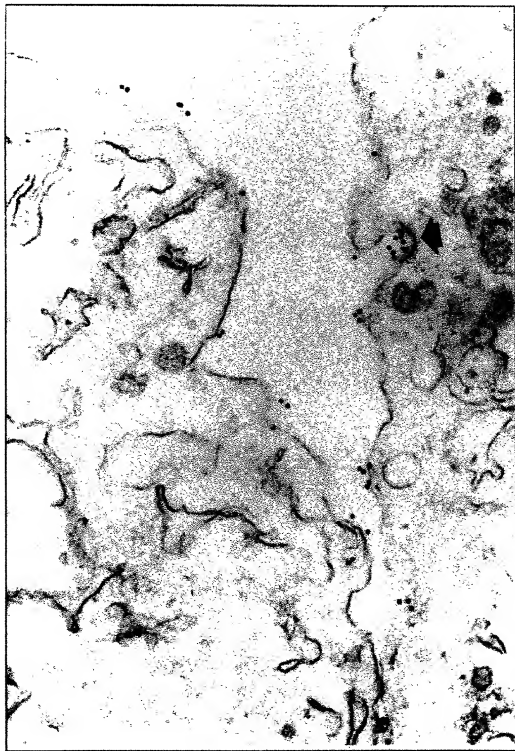


FIG. 2

03/12



FIG. 3

402021-01000000

04/12

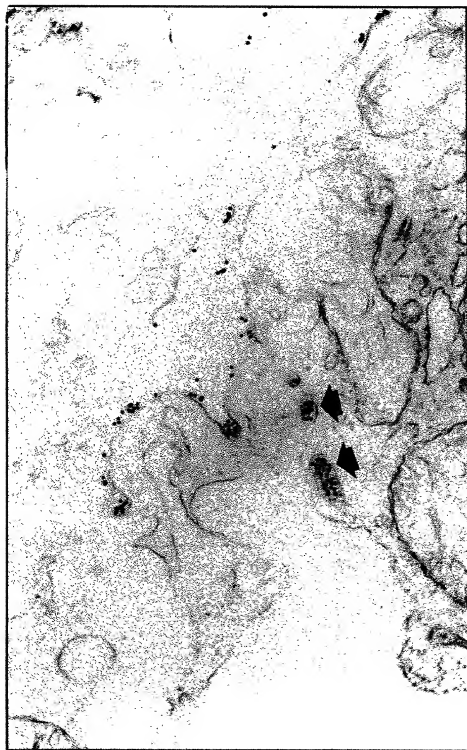


FIG. 4

00020546-126776
102001-54502600

05/12

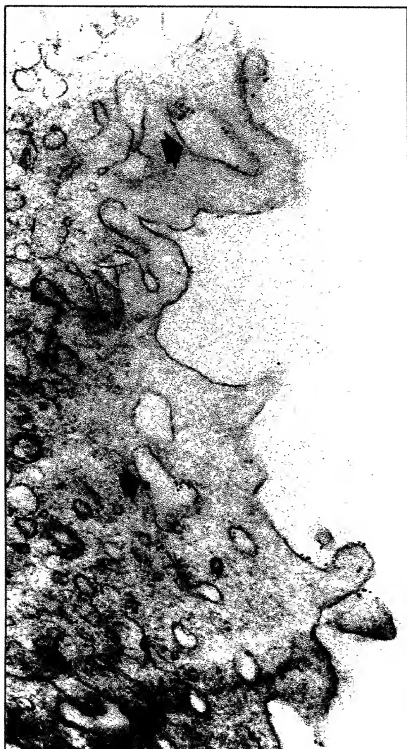


FIG. 5

06/12

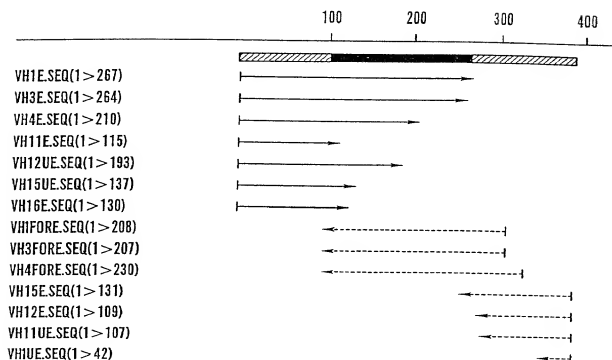


FIG. 6

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE



08/12

LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115)	SEQ2(1>125)	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
J591VH.PRO	MUVHIA.PRO				
(1>115)	(1>125)	75.6	2	10	125

```

      10      20      30      40      50
EVQLQQSGPELVKPGISVRISCKTSGYTFTEYTI-HWVKQSHGKSLIEWIGNINPNNGGIT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFY:Y: :VVKQS.GKSLIEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFIDYAMNNVVKQSPGKSLIEWIGDINPGGGIS
      10      20      30      40      50      60
YNQKPFEDKATLTVDKSSSTAYMELRSLTSEDGAVYYCAAG-----VNFEDYWGQGIT
YNQKF.:KATLTVDKSSSTAYM:L.SLTSEDGAVYYCA G .FDYWGQGIT
YNQKPFKATLTVDKSSSTAYMQLSSLTSEDGAVYYCARGYSSSYMAYYFDYWGQGIT
      70      80      90      100      110      120

```

LIVSS
:IVSS
VIVSS

FIG. 8

09/12

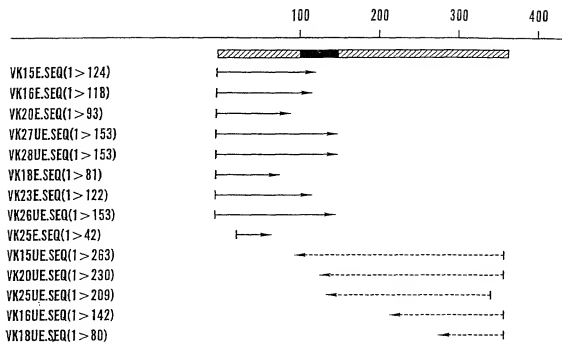


FIG. 9

10/12

ENZYMES: ALL 74 ENZYMES (NO FILTER):
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

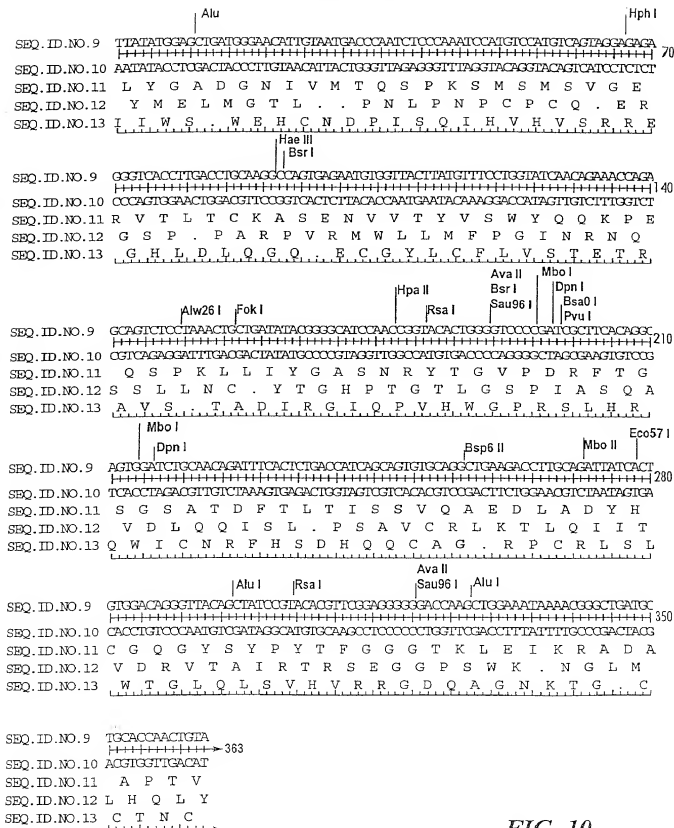


FIG. 10

11/12

LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO	SEQ2(1 > 1 1 1) MUVKV.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>107)	(1>109)	60.4	2	2	109

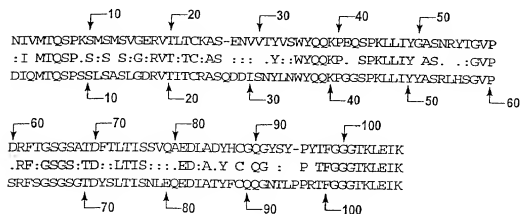


FIG. 11

